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RAW SEQUENCE LISTING

DATE: 08/29/2002

PATENT APPLICATION: US/09/909,566C

TIME: 13:41:29

Input Set : A:\BB1465 US NA substitute seq 1st..txt

Output Set: N:\CRF3\08292002\I909566C.raw

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3 <110> APPLICANT: Cahoon, Edgar B
 5 <120> TITLE OF INVENTION: A Cytochrome P450 enzyme associated with the synthesis of
 delta-
 6 12-epoxy fatty acids
 8 <130> FILE REFERENCE: BB1465 US NA
 10 <140> CURRENT APPLICATION NUMBER: 09/909566C
 11 <141> CURRENT FILING DATE: 2001-07-20
 13 <150> PRIOR APPLICATION NUMBER: 60/219833
 14 <151> PRIOR FILING DATE: 2000-07-21
 16 <160> NUMBER OF SEQ ID NOS: 7
 18 <170> SOFTWARE: Microsoft Office 97
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 1733
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Euphorbia lagascae
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 27 gcttggtttta atcttagtag tagtcatgag gttgtggaag aaacagaatc cacctccagg 120
 28 gccatggaag ttctctatca taggtaatct tcctcattta ttactcactt ctgatctagg 180
 29 ccatgaacgt tttagagcct tggctcaaat ttatggacct gttatgagtc ttcaaattgg 240
 30 ccaagtttca gctgttgta tttcttcagc tgaagcagcc aaagagggtta tgaaaactca 300
 31 ggctgatgcc ttgcgccaac gccctatcgt cttggacgca cagatttgtgt ttataaatcg 360
 32 gaaagatgtc ttgtttgctt catatggaga tcaactggagg cagatgaaga aaatttggat 420
 33 acttgaattt ctgagtgcc aaaaagttca atcctccagg ttaatccgag aggaagaaat 480
 34 ggaggatgcc atcacattcc tccgttcgaa agccgatct cgggtcaata ttacaaagat 540
 35 catttatggc attataattt cgatcatgat aagaacatcc gttggttaatt gtaagcaaaa 600
 36 agaaagattg ctgagtgttg ccgatgcagt caatgaggca gcgacgagtt ttggcaccgc 660
 37 agacgctttt ccgacgtgga aattacttca ctatatcatt ggagctgagt caaaaccag 720
 38 gcgtttgcat caggagattg acgatatact tgaagagatt cttaatgaac acaaagccaa 780
 39 taagcctttt gaagcggata acttaatgga tgttctattg aatcttcaaa aaaatggaaa 840
 40 cgttccagtg ccagtgacaa acgaaagcat caaagcatcc gttttgcaaa tgtttactgc 900
 41 cgggagcgaa acaacttcga aagctacaga atgggtaatg gcagagctga tgaaaaatcc 960
 42 aactgaacta agaaaagcac aagaagaagt tagacaagta tttggtgaaa tgggaaaagt 1020
 43 tgatgaatca agatttcatg atttgaaatt cttcaagtta gtggttaaag aaactctaag 1080
 44 attacatcct ccggttgtct tgattccgag ggagtgtaga gaaacaacac gaattgatgg 1140
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 51 ctcaaataat tcttgattac ataggagggt tgaaatatat ataataaact ttaattaacg 1560
 52 atgttcta atgtgttggg tgagttataa taggttttcc accgatcata taagtgcct 1620
 53 tctttgatgg atgggttaga ttataatgag ttgtgggttg gatttttaga tgggttaaat 1680

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60 <213> ORGANISM: Euphorbia lagascae
62 <400> SEQUENCE: 2
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64   1             5             10             15
66 Leu Val Leu Ile Leu Val Val Val Met Arg Leu Trp Lys Lys Gln Asn
67             20             25             30
69 Pro Pro Pro Gly Pro Trp Lys Phe Pro Ile Ile Gly Asn Leu Pro His
70             35             40             45
72 Leu Leu Leu Thr Ser Asp Leu Gly His Glu Arg Phe Arg Ala Leu Ala
73             50             55             60
75 Gln Ile Tyr Gly Pro Val Met Ser Leu Gln Ile Gly Gln Val Ser Ala
76   65             70             75             80
78 Val Val Ile Ser Ser Ala Glu Ala Ala Lys Glu Val Met Lys Thr Gln
79             85             90             95
81 Ala Asp Ala Phe Ala Gln Arg Pro Ile Val Leu Asp Ala Gln Ile Val
82             100            105            110
84 Phe Tyr Asn Arg Lys Asp Val Leu Phe Ala Ser Tyr Gly Asp His Trp
85             115            120            125
87 Arg Gln Met Lys Lys Ile Trp Ile Leu Glu Phe Leu Ser Ala Lys Lys
88             130            135            140
90 Val Gln Ser Ser Arg Leu Ile Arg Glu Glu Glu Met Glu Asp Ala Ile
91   145            150            155            160
93 Thr Phe Leu Arg Ser Lys Ala Gly Ser Pro Val Asn Ile Thr Lys Ile
94             165            170            175
96 Ile Tyr Gly Ile Ile Ile Ser Ile Met Ile Arg Thr Ser Val Gly Asn
97             180            185            190
99 Cys Lys Gln Lys Glu Arg Leu Leu Ser Val Ala Asp Ala Val Asn Glu
100            195            200            205
102 Ala Ala Thr Ser Phe Gly Thr Ala Asp Ala Phe Pro Thr Trp Lys Leu
103            210            215            220
105 Leu His Tyr Ile Ile Gly Ala Glu Ser Lys Pro Arg Arg Leu His Gln
106   225            230            235            240
108 Glu Ile Asp Asp Ile Leu Glu Glu Ile Leu Asn Glu His Lys Ala Asn
109            245            250            255
111 Lys Pro Phe Glu Ala Asp Asn Leu Met Asp Val Leu Leu Asn Leu Gln
112            260            265            270
114 Lys Asn Gly Asn Val Pro Val Pro Val Thr Asn Glu Ser Ile Lys Ala
115            275            280            285
117 Ser Val Leu Gln Met Phe Thr Ala Gly Ser Glu Thr Thr Ser Lys Ala
118            290            295            300
120 Thr Glu Trp Val Met Ala Glu Leu Met Lys Asn Pro Thr Glu Leu Arg
121   305            310            315            320
123 Lys Ala Gln Glu Glu Val Arg Gln Val Phe Gly Glu Met Gly Lys Val
124            325            330            335
126 Asp Glu Ser Arg Phe His Asp Leu Lys Phe Phe Lys Leu Val Val Lys

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127          340          345          350
129 Glu Thr Leu Arg Leu His Pro Pro Val Val Leu Ile Pro Arg Glu Cys
130          355          360          365
132 Arg Glu Thr Thr Arg Ile Asp Gly Tyr Glu Ile His Pro Asn Thr Arg
133          370          375          380
135 Ile Val Val Asn Ala Trp Ala Ile Gly Arg Asp Pro Asn Thr Trp Ser
136 385          390          395          400
138 Glu Pro Gly Lys Phe Asn Pro Glu Arg Phe Lys Asp Cys Ala Ile Asp
139          405          410          415
141 Tyr Lys Gly Thr Phe Glu Leu Val Pro Phe Gly Ala Gly Lys Arg
142          420          425          430
144 Ile Cys Pro Gly Ile Thr Ser Ala Ile Thr Asn Leu Glu Tyr Val Ile
145          435          440          445
147 Ile Asn Leu Leu Tyr His Phe Asn Trp Glu Leu Ala Asp Gly Ile Thr
148          450          455          460
150 Pro Gln Thr Leu Asp Met Thr Glu Ala Ile Gly Gly Ala Leu Arg Lys
151 465          470          475          480
153 Lys Ile Asp Leu Lys Leu Ile Pro Ile Pro Tyr Gln Val Ser Leu Gly
154          485          490          495
156 Ser Asn Ile Ser
157          500
160 <210> SEQ ID NO: 3
161 <211> LENGTH: 502
162 <212> TYPE: PRT
163 <213> ORGANISM: Capsicum annuum
165 <400> SEQUENCE: 3
166 Met Glu Ile Gln Phe Thr Asn Leu Val Ala Phe Leu Leu Phe Leu Ser
167 1          5          10          15
169 Ser Ile Ile Leu Leu Leu Lys Lys Trp Lys Thr Gln Lys Leu Asn Leu
170          20          25          30
172 Pro Pro Gly Pro Trp Lys Leu Pro Phe Ile Gly Ser Leu His His Leu
173          35          40          45
175 Ala Val Ala Gly Pro Leu Pro His His Gly Leu Lys Asn Leu Ala Lys
176          50          55          60
178 Leu Tyr Gly Pro Leu Met His Leu Arg Leu Gly Glu Ile Pro Thr Val
179 65          70          75          80
181 Ile Ile Ser Ser Pro Arg Met Ala Lys Glu Val Leu Lys Thr His Asp
182          85          90          95
184 Leu Ala Phe Ala Thr Arg Pro Lys Leu Val Val Ala Asp Ile Val His
185          100          105          110
187 Tyr Asp Ser Thr Asp Ile Ala Phe Ser Pro Tyr Gly Glu Tyr Trp Arg
188          115          120          125
190 Gln Ile Arg Lys Ile Cys Ile Leu Glu Leu Leu Ser Ala Lys Met Val
191          130          135          140
193 Lys Phe Phe Ser Ser Ile Arg Gln Asp Glu Leu Ser Met Met Val Ser
194 145          150          155          160
196 Ser Ile Arg Thr Met Pro Asn Phe Pro Val Asn Leu Thr Asp Lys Ile
197          165          170          175
199 Phe Trp Phe Thr Ser Ser Val Thr Cys Arg Ser Ala Leu Gly Lys Ile

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200          180          185          190
202 Cys Arg Asp Gln Asp Lys Leu Ile Ile Phe Met Arg Glu Ile Ile Ser
203          195          200          205
205 Leu Thr Gly Gly Phe Ser Ile Ala Asp Phe Phe Pro Thr Trp Lys Met
206          210          215          220
208 Leu His Asp Val Gly Gly Ser Lys Thr Arg Leu Leu Lys Ala His Arg
209 225          230          235          240
211 Lys Ile Asp Glu Ile Leu Glu His Val Val Asn Glu His Lys Gln Asn
212          245          250          255
214 Arg Ala Asp Gly Gln Lys Gly Asn Gly Glu Phe Gly Gly Glu Asp Leu
215          260          265          270
217 Ile Asp Val Leu Leu Arg Val Arg Glu Ser Gly Glu Val Gln Ile Ser
218          275          280          285
220 Ile Thr Asp Asp Asn Ile Lys Ser Ile Leu Val Asp Met Phe Ser Ala
221          290          295          300
223 Gly Ser Glu Thr Ser Ser Thr Thr Ile Ile Trp Ala Leu Ala Glu Met
224 305          310          315          320
226 Met Lys Lys Pro Ser Val Leu Ala Lys Ala Gln Ala Glu Val Arg Gln
227          325          330          335
229 Val Leu Lys Glu Lys Lys Gly Phe Gln Gln Ile Asp Leu Asp Glu Leu
230          340          345          350
232 Lys Tyr Leu Lys Leu Val Ile Lys Glu Thr Leu Arg Met His Pro Pro
233          355          360          365
235 Ile Pro Leu Leu Val Pro Arg Glu Cys Met Lys Asp Thr Lys Ile Asp
236          370          375          380
238 Gly Tyr Asn Ile Pro Phe Lys Thr Arg Val Ile Val Asn Ala Trp Ala
239 385          390          395          400
241 Ile Gly Arg Asp Pro Glu Ser Trp Asp Asp Pro Glu Ser Phe Ser Pro
242          405          410          415
244 Glu Arg Phe Glu Asn Ser Ser Val Asp Phe Leu Gly Ser His His Gln
245          420          425          430
247 Phe Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Pro Gly Met Leu Phe
248          435          440          445
250 Gly Leu Ala Asn Val Gly Gln Pro Leu Ala Gln Leu Leu Tyr His Phe
251          450          455          460
253 Asp Arg Lys Leu Pro Asn Gly Gln Ser His Glu Asn Leu Asp Met Thr
254 465          470          475          480
256 Glu Ser Pro Gly Ile Ser Ala Thr Arg Lys Asp Asp Leu Val Leu Ile
257          485          490          495
259 Ala Thr Pro Tyr Asp Pro
260          500
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264 <211> LENGTH: 51
265 <212> TYPE: DNA
266 <213> ORGANISM: artificial sequence
268 <220> FEATURE:
269 <221> NAME/KEY: misc_feature
270 <222> LOCATION:
271 <223> OTHER INFORMATION: oligonucleotide primer

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278 <211> LENGTH: 35
279 <212> TYPE: DNA
280 <213> ORGANISM: artificial sequence
282 <220> FEATURE:
283 <221> NAME/KEY: misc_feature
284 <222> LOCATION:
285 <223> OTHER INFORMATION: oligonucleotide primer
287 <400> SEQUENCE: 5
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291 <210> SEQ ID NO: 6
292 <211> LENGTH: 35
293 <212> TYPE: DNA
294 <213> ORGANISM: artificial sequence
296 <220> FEATURE:
297 <221> NAME/KEY: misc_feature
298 <222> LOCATION:
299 <223> OTHER INFORMATION: oligonucleotide primer
301 <400> SEQUENCE: 6
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306 <211> LENGTH: 35
307 <212> TYPE: DNA
308 <213> ORGANISM: artificial sequence
310 <220> FEATURE:
311 <221> NAME/KEY: misc_feature
312 <222> LOCATION:
313 <223> OTHER INFORMATION: oligonucleotide primer
315 <400> SEQUENCE: 7
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VERIFICATION SUMMARY

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